> This Raw Listing contains the General
> Information Section and up to the first 5 pages.

```
  1                              SEQUENCE LISTING
  2
  3   (1)    General Information
  4
  5          (i) APPLICANT: BILLING-MEDEL, PATRICIA          ENTERED
  6                         COHEN, MAURICE
  7                         COLPITTS, TRACEY L.
  8                         FRIEDMAN, PAULA N.
  9                         GORDON, JULIAN
 10                         GRANADOS, EDWARD N.
 11                         HODGES, STEVEN C.
 12                         KLASS, MICHAEL R.
 13                         KRATOCHVIL, JON D.
 14                         RUSSELL, JOHN C.
 15                         STROUPE, STEPHEN D.
 16                         YU, HONG
 17
 18
 19          (ii) TITLE OF THE INVENTION: METHODS AND REAGENTS USEFUL
 20                    FOR DETECTING DISEASES OF THE BREAST
 21
 22          (iii) NUMBER OF SEQUENCES: 37
 23
 24          (iv) CORRESPONDENCE ADDRESS:
 25             (A) ADDRESSEE: Abbott Laboratories
 26             (B) STREET: 100 Abbott Park Road
 27             (C) CITY: Abbott Park
 28             (D) STATE: IL
 29             (E) COUNTRY: USA
 30             (F) ZIP: 60064-3500
 31
 32          (v) COMPUTER READABLE FORM:
 33             (A) MEDIUM TYPE: Diskette
 34             (B) COMPUTER: IBM Compatible
 35             (C) OPERATING SYSTEM: DOS
 36             (D) SOFTWARE: FastSEQ for Windows Version 2.0
 37
 38          (vi) CURRENT APPLICATION DATA:
 39             (A) APPLICATION NUMBER:
 40             (B) FILING DATE:
 41             (C) CLASSIFICATION:
 42
 43          (vii) PRIOR APPLICATION DATA:
 44             (A) APPLICATION NUMBER: 08/889,127
 45             (B) FILING DATE: 07-JUL-1997
 46
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47
48
49          (viii) ATTORNEY/AGENT INFORMATION:
50             (A) NAME: Becker, Cheryl L.
51             (B) REGISTRATION NUMBER: 35,441
52             (C) REFERENCE/DOCKET NUMBER: 6130.US.P1
53
54          (ix) TELECOMMUNICATION INFORMATION:
55             (A) TELEPHONE: 847/935-1729
56             (B) TELEFAX: 847/938-2623
57             (C) TELEX:
58
59
60             (2) INFORMATION FOR SEQ ID NO:1:
61
62          (i) SEQUENCE CHARACTERISTICS:
63             (A) LENGTH: 270 base pairs
64             (B) TYPE: nucleic acid
65             (C) STRANDEDNESS: single
66             (D) TOPOLOGY: linear
67
68
69          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
70
71     GTCACCACCA TCAGGACAAG TGTAACCTTT AAGCTAAATG AAGGCAAGTG TAGTTTGAAA        60
72     AATGCTGAGC TGTTTCCCGA GGGTCTGCGA CCAGCACTAC CAGAGAAGCA CAGCTCAGTA       120
73     AAAGAGAGCT TCCGCTACGT AAACCTTACA TGCAGCTCTG GCAAGCAAGT CCCAGGAGCC       180
74     CCTGGCCGAC CAAGCACCCC TAAGGAAATG TTTATCACTG TTGAGTTTGA GCTTGAAACT       240
75     AACCAAAAGG AGGTGACAGC TTCTTGTGAC                                        270
76
77             (2) INFORMATION FOR SEQ ID NO:2:
78
79          (i) SEQUENCE CHARACTERISTICS:
80             (A) LENGTH: 275 base pairs
81             (B) TYPE: nucleic acid
82             (C) STRANDEDNESS: single
83             (D) TOPOLOGY: linear
84
85
86          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
87
88     GGAAATGTTT ATCACTGTTG AGTTTGAGCT TGAAACTAAC CAAAAGGAGG TGACAGCTTC        60
89     TTGTGACCTG AGCTGCATCG TAAAGCGAAC CGAGAAGCGG CTCCGTAAAG CCATCCGCAT       120
90     GCTCAGAAAG GCCGTCCACA GGGAGCAGTT TCACCTCCAG CTCTCAGGCA TGAACCTCGA       180
91     CGTGGCTAAA AAGCCTCCCA GAACATCTGA ACGCCAGGCA GAGTCCTGTG GAGTGGGCCA       240
92     GGGTCATGCA GAAAACCAAT GTGTCAGTTG CAGGG                                  275
93
94             (2) INFORMATION FOR SEQ ID NO:3:
95
96          (i) SEQUENCE CHARACTERISTICS:
97             (A) LENGTH: 254 base pairs
98             (B) TYPE: nucleic acid
99             (C) STRANDEDNESS: single
```

```
100              (D) TOPOLOGY: linear
101
102
103         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
104
105     AGCGGCTCCG TAAAGCCATC CGCACGCTCA GAAAGGCCGT CCACAGGGAG CAGTTTCACC     60
106     TCCAGCTCTC AGGCATGAAC CTCGACGTGG CTAAAAAGCC TCCCAGAACA TCTGAACGCC    120
107     AGGCAGAGTC CTGTGGAGTG GGCCAGGGTC ATGCAGAAAA CCAATGTGTC AGTTGCAGGG    180
108     CTGGGACCTA TTATGATGGA GCACGAGAAC GCTGCATTTT ATGTCCAAAT GGAACCTTCC    240
109     AAAATGAGGA AGGA                                                      254
110
111             (2) INFORMATION FOR SEQ ID NO:4:
112
113         (i) SEQUENCE CHARACTERISTICS:
114             (A) LENGTH: 225 base pairs
115             (B) TYPE: nucleic acid
116             (C) STRANDEDNESS: single
117             (D) TOPOLOGY: linear
118
119
120         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
121
122     GGAAGGACAA ATGACTTGTG AACCATGCCC AAGACCAGGA AATTCTGGGG CCCTGAAGAC     60
123     CCCAGAAGCT TGGAATATGT CTGAATGTGG AGGTCTGTGT CAACCTGGTG AATATTCTGC    120
124     AGATGGCTTT GCACCTTGCC AGCTCTGTGC CCTGGGCACG TTCCAGCCTG AAGCTGGTCG    180
125     AACTTCCTGC TTCCCCTGTG GAGGAGGCCT TGCCACCAAA CATCA                    225
126
127             (2) INFORMATION FOR SEQ ID NO:5:
128
129         (i) SEQUENCE CHARACTERISTICS:
130             (A) LENGTH: 245 base pairs
131             (B) TYPE: nucleic acid
132             (C) STRANDEDNESS: single
133             (D) TOPOLOGY: linear
134
135         (ix) FEATURE:
136             (A) NAME/KEY: base_polymorphism
137             (B) LOCATION: 91
138             (D) OTHER INFORMATION: /note= " N' represents an A or G or
139                     T or C polymorphism at this position"
140
141         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
142
143     CTGTGGAGGA GGCCTTGCCA CCAAACATCA GGGAGCTACT TCCTTTCAGG ACTGTGAAAC     60
144     CAGAGTTCAA TGTTCACCTG GACATTTCTA NAACACCACC ACTCACCGAT GTATTCGTTG    120
145     CCCAGTGGGA ACATACCAGC CTGAATTTGG AAAAAATAAT TGTGTTTCTT GCCCAGGAAA    180
146     TACTACGACT GACTTTGATG GCTCCACAAA CATAACCCAG TGTAAAAACA GAAGATGTGG    240
147     AGGGG                                                               245
148
149             (2) INFORMATION FOR SEQ ID NO:6:
150
151         (i) SEQUENCE CHARACTERISTICS:
152             (A) LENGTH: 206 base pairs
```

```
153            (B) TYPE: nucleic acid
154            (C) STRANDEDNESS: single
155            (D) TOPOLOGY: linear
156
157
158        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
159
160    GTTCACCTGG ACATTTCTAC AACACCACCA CTCACCGATG TATTCGTTGC CCAGTGGGAA        60
161    CATACCAGCC TGAATTTGGA AAAAATAATT GTGTTTCTTG CCCAGGAAAT ACTACGACTG       120
162    ACTTTGATGG CTCCACAAAC ATAACCCAGT GTAAAAACAG AAGATGTGGA GGGGAGCTGG       180
163    GAGATTTCAC TGGGTACATT GAATCC                                           206
164
165        (2) INFORMATION FOR SEQ ID NO:7:
166
167        (i) SEQUENCE CHARACTERISTICS:
168            (A) LENGTH: 181 base pairs
169            (B) TYPE: nucleic acid
170            (C) STRANDEDNESS: single
171            (D) TOPOLOGY: linear
172
173        (ix) FEATURE:
174            (A) NAME/KEY: base_polymorphism
175            (B) LOCATION: 55
176            (D) OTHER INFORMATION: /note= " N' represents an A or G or
177                    T or C polymorphism at this position"
178
179        (ix) FEATURE:
180            (A) NAME/KEY: base_polymorphism
181            (B) LOCATION: 162
182            (D) OTHER INFORMATION: /note= " N' represents an A or G or
183                    T or C polymorphism at this position"
184
185        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
186
187    TGAATCCCCA AACTACCCAG GCAATTACCC AGCCAACACC GAGTGTACGT GGACNATCAA        60
188    CCCACCCCCC AAGCGCCGCA TCCTGATCGT GGTCCCTGAG ATCTTCCTGC CCATAGAGGA       120
189    CGACTGTGGG GACTATCTGG TGATGCGGAA AACCTCTTCA TNCAATTCTG TGACAACATA       180
190    T                                                                     181
191
192        (2) INFORMATION FOR SEQ ID NO:8:
193
194        (i) SEQUENCE CHARACTERISTICS:
195            (A) LENGTH: 280 base pairs
196            (B) TYPE: nucleic acid
197            (C) STRANDEDNESS: single
198            (D) TOPOLOGY: linear
199
200        (ix) FEATURE:
201            (A) NAME/KEY: base_polymorphism
202            (B) LOCATION: 81
203            (D) OTHER INFORMATION: /note= " N' represents an A or G or
204                    T or C polymorphism at this position"
205
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206             (ix) FEATURE:
207                  (A) NAME/KEY: base_polymorphism
208                  (B) LOCATION: 125
209                  (D) OTHER INFORMATION: /note= " N' represents an A or G or
210                          T or C polymorphism at this position"
211
212             (ix) FEATURE:
213                  (A) NAME/KEY: base_polymorphism
214                  (B) LOCATION: 174
215                  (D) OTHER INFORMATION: /note= " N' represents an A or G or
216                          T or C polymorphism at this position"
217
218          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
219
220   CAACATATGA AACCTGCCAG ACCTACGAAC GCCCCATCGC CTTCACCTCC AGGTCAAAGA       60
221   AGCTGTGGAT TCAGTTCAAG NCCAATGAAG GGAACAGCGC TAGAGGGTTC CAGGTCCCAT      120
222   ACGTNACATA TGATGAGGAC TACCAGGAAC TCATTGAAGA CATAGTTCGA GATNGCAGGC      180
223   TCTATGCATC TGAGAACCAT CAGGAAATAC TTAAGGATAA GAAACTTATC AAGGCTCTGT      240
224   TTGATGTCCT GGCCCATCCC CAGAACTATT TCAAGTACAC                            280
225
226          (2) INFORMATION FOR SEQ ID NO:9:
227
228          (i) SEQUENCE CHARACTERISTICS:
229             (A) LENGTH: 261 base pairs
230             (B) TYPE: nucleic acid
231             (C) STRANDEDNESS: single
232             (D) TOPOLOGY: linear
233
234          (ix) FEATURE:
235              (A) NAME/KEY: base_polymorphism
236              (B) LOCATION: 79
237              (D) OTHER INFORMATION: /note= " N' represents an A or G or
238                          T or C polymorphism at this position"
239
240          (ix) FEATURE:
241              (A) NAME/KEY: base_polymorphism
242              (B) LOCATION: 258
243              (D) OTHER INFORMATION: /note= " N' represents an A or G or
244                          T or C polymorphism at this position"
245
246          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
247
248   GAAACTTATC AAGGCTCTGT TTGATGTCCT GGCCCATCCC CAGAACTATT TCAAGTACAC       60
249   AGCCCAGGAG TCCCGAGANA TGTTTCCAAG ATCGTTCATC CGATTGCTAC GTTCCAAAGT      120
250   GTCCAGGTTT TTGAGACCTT ACAAATGACT CAGCCCACGT GCCACTCAAT ACAAATGTTC      180
251   TGCTATAGGG TTGGTGGGAC AGAGCTGTCT TCCTTCTGCA TGTCAGCACA GTCGGGTATT      240
252   GCTGCCTCCC GTATCAGNGA C                                                261
253
254          (2) INFORMATION FOR SEQ ID NO:10:
255
256          (i) SEQUENCE CHARACTERISTICS:
257             (A) LENGTH: 282 base pairs
258             (B) TYPE: nucleic acid
```

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/09/110,720*

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Line	Error	Original Text
16	Response Exceeds Line Limitations	YU, HONG